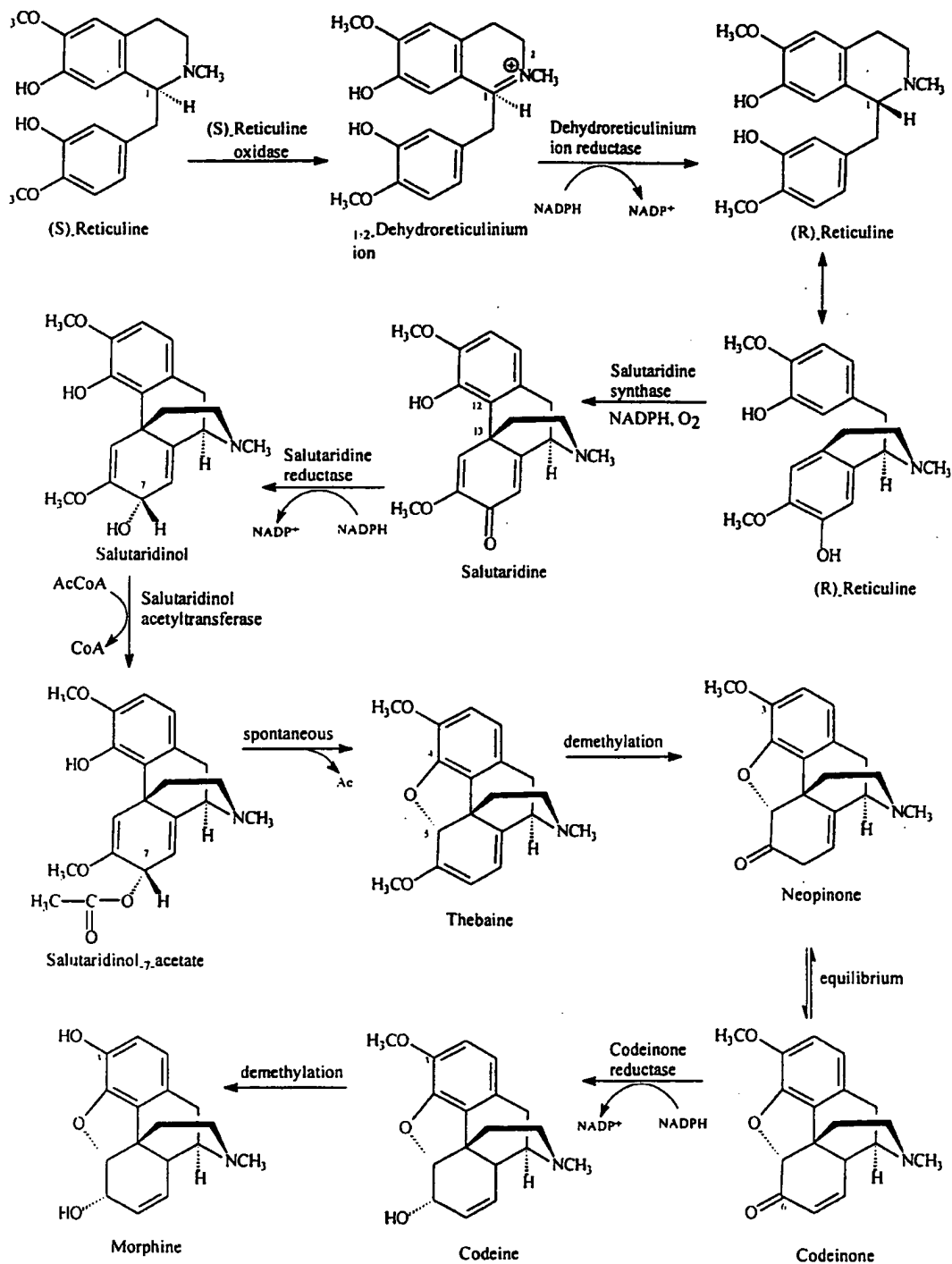


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Fig 1

SCHEME I



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Fig 2

Peptide 3	X L Q E L M A
Peptide 7	V L H Q I A V A R G K
Peptide 14	D D D E L F I T S K
Peptide 16	I P D V V N Q V E M S P T L G Q
Peptide 17	X V N E I P K
Peptide 25	X V A Q V
Peptide 29	I F D N X L T A E D

Fig 3

	51		90
Alfalfa	KQGYRHFDTA	AAYGSEQALG	EALKEAIELG LVTREELFVT
Glycyrrh.	KQGYRHFDTA	AAYGSETALG	EALKEARDLG LVTREELFVT
Soybean	KQGYRHFDTA	AAYGSEQALG	EALKEAIHLG LVSRQDLFVT
Opium poppyELFIT
	91		140
	SKLWVTENHP	HLVIPALQKS	LKTLQLDYLD LYLIHWPLSS QPGKFSFPID
	SKLWVTENHP	HLVIPALRKS	LETQLLEYLD LYLIHWPLSS QPGKFSFPIQ
	SKLWVTENHP	HLVLPALRKS	LKTLQLLEYLD LYLIHWPLSS QPGKFSFPIE
	SK.....
	141		190
	VADLLPFDVK	GVWESMEESL	KLGLTKAIGV SNFSVKKLEN LLSVATVLPA
	VEDLLPFDVK	GVWESMEECL	KLGLTKAIGV SNFSVKKLQN LLSVATIRPA
	VEDLLPFDVK	GVWESMEECQ	KLGLTKAIGV SNFSVKKLQN LLSVATIRPV
LQE LMA...IPDV
	191		240
	VNQVEMN...	LAWQQKKLRE	FCNANGIVLT AFSPLRKGAS RGPNEVMEND
	VNQVEMN...	LAWQQKKLRE	FCTANGIVLT AFSPLRKGAS RGPNEVMEND
	VDQVEMN...	LAWQQKKLRE	FCKENGIIVT AFSPLRKGAS RGPNEVMEND
	VNQVEMSPTL.....
	241		
	MLKEIADAHG	KSVAQISLRW	LYEQGVTFVP KSYDKERMNQ NLC
	MLKGIAEAHG	KSIAQVSLRW	LYEQGVTFVA KSYDKERMNQ NLQ
	VLKEIAEAHG	KSIAQVSLRW	LYEQGVTFVP KSYDKERMNQ NLH
	VLHQIAVARG	K.....VNEIP K.....

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Fig 4

```

cor1.1 .MESNGVPMI TLSSG...IR MPALGMGTAE TMVKGTEREK LAFLKAIEVG
cor1.2 -----V- --E----- --N-----
cor1.3 -----
cor1.4 -----
6'dcs MAAAIEI-T- VFPNSSAQQ- --VV---S-P DFTCKKDT.- E-IIE-VKQ-

```

```

cor1.1 YRHFDTAAY QTEECLEAI AEALQLGLIK SRDELFITSK LWCADAHADL
cor1.2 -----S-----
cor1.3 -----S-----
cor1.4 -----S-----
6'dcs -----GS-QA----L K-IH---VS .-QD-V---- --VTEN-PH-

```

```

cor1.1 VLPALQNSLR NLKLDYLDLY LIHHPVSLKP GKFVNEIPKD HILPMDYKSV
cor1.2 -----E----- --L-----
cor1.3 -----
cor1.4 -----E-----
6'dcs -----RK--K T-Q-E----- --W-L-SQ- ---SFP-EVE DL--F-V-G-

```

```

cor1.1 WAAMEECQTL GFTRAIGVCN FSCKRLQELM ETANSPPVVN QVEMSPTLHQ
cor1.2 -----S----- --K----- A--KI-----
cor1.3 ----- --K----- AA-KI-----
cor1.4 -----S----- --K----- AA-KI-----
6'dcs -ES-----K- -L-K---S- --V-K--N-L SV-TIR---D ----NLAWQ-

```

```

cor1.1 KNLREYCKAN NIMITAHSVL GAVGAAWGTN AVMHKSVLHQ IAVARGKSV
cor1.2 ----- --I--P--S- ---D-----
cor1.3 ----- --IC-P--S- ---D-----
cor1.4 ----- --I--P--S- ---D-----
6'dcs -K---F--E- G-IV--F-P- .RK--SR-P- E--END--KE --E-H---I-

```

```

cor1.1 QVSMRWVYQQ GASLVVKSFN EARMKENLKI FDWELTAEDM EKISEIPQSR
cor1.2 ----- --S-----
cor1.3 ----- -G----- --N-----
cor1.4 ----- -G-----
6'dcs ---L--L-E- -VTF-P--YD KE--NQ--H- ---A--EQ-H H--Q-S--

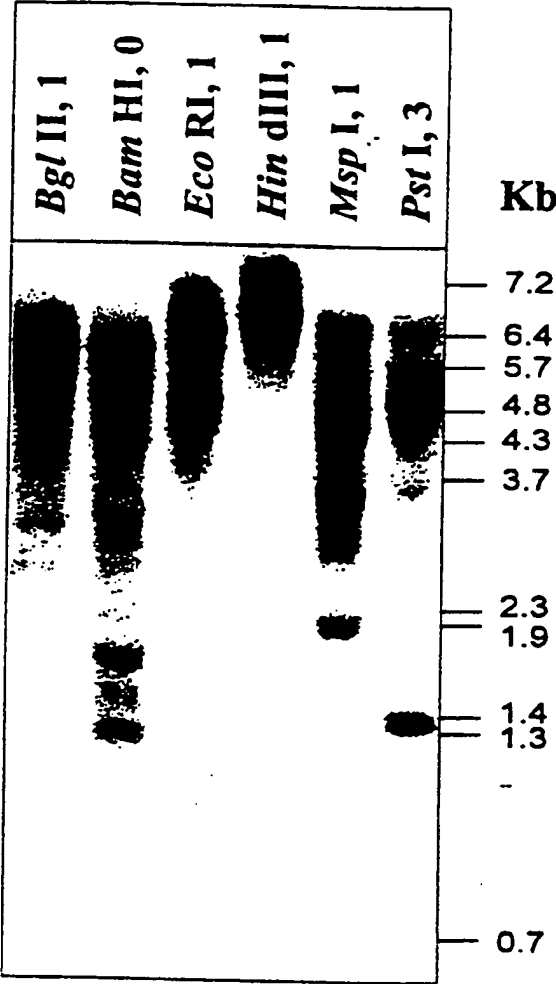
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```

cor1.1 TSSAAFLSP TGPFKTEEF WDEKD
cor1.2 ----D-----
cor1.3 ----D-----
cor1.4 -----
6'dcs .....LISG- -K-..QLADL --DQI

```

FIGURE 5



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FIGURE 6

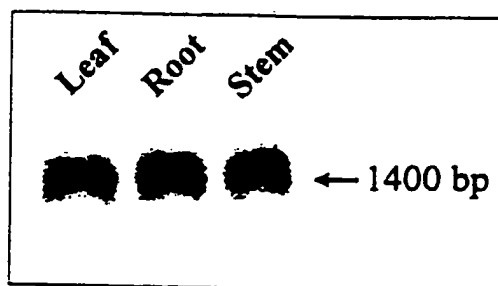
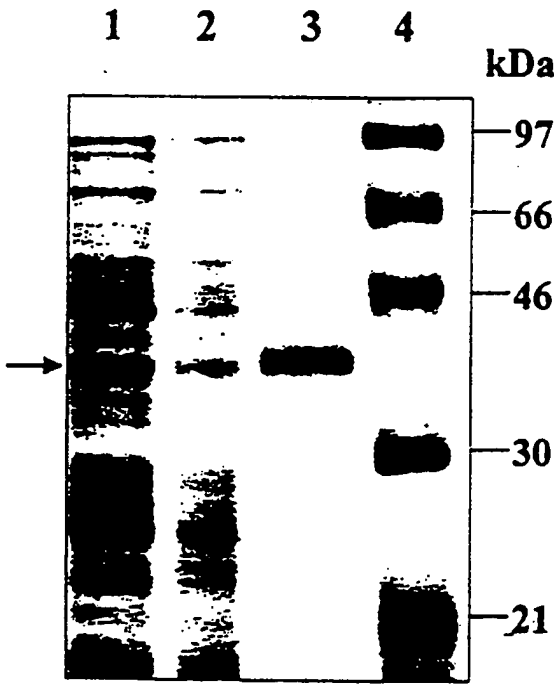
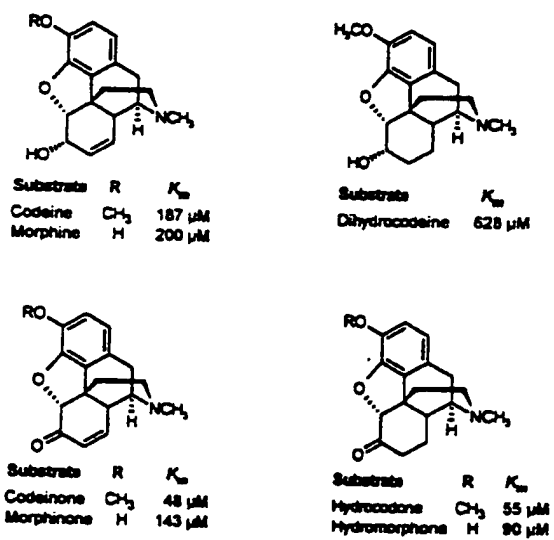


FIGURE 7



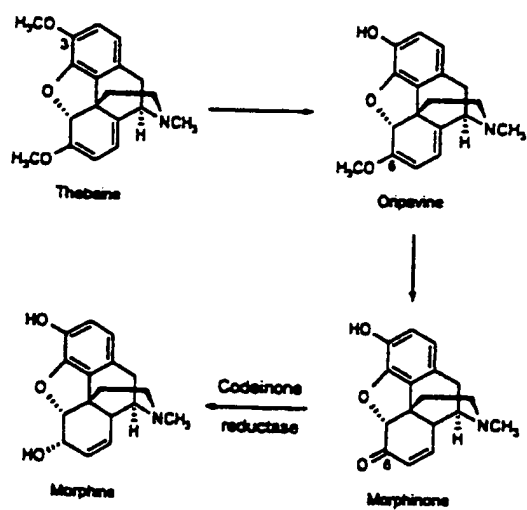
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FIGURE 8



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FIGURE 9



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cor1.1
cds6-971

Fig 10

GAAAAATGGAGAGTAATGGTGTACCTATGATCACTCTCAGTTCCGGCATTCCGGATGCCTGCTTTAGGTATGGGAA
CAGCTGAAACAATGGTAAAAGGAACAGAAAGAGAGAAATTGGCGTTTTTGAAGCGATAGAGGTCGGTTACAGAC
ACTTCGATACAGCTGCTGCATACCAAAGTGAAGAGTGTCTTGGTGAAGCTATAGCTGAAGCACTTCAACTTGGTC
TAATAAAATCTCGAGATGAACCTTTCATCACTTCCAAGCTCTGGTGGCTGATGCTCAGCTGATCTTGTCTCTCC
CTGCTCTTCAGAATTCTCTGAGGAATCTTAAATTGGACTATCTTGATCTATATTTGATACACCATCCGGTAAGCT
TGAAGCCAGGGAAGTTTGTAAACGAAATACCAAAGGATCATATCCTTCCAATGGACTACAAATCTGTATGGGCAG
CCATGGGAAGAGTGTGAGACCCTTGGCTTCACTAGGGCAATCGGGGTCTGTAATTTCTCATGCAAAAAGGCTTCAAG
AGTTGATGGAAACAGCCAACAGCCCTCCAGTTGTGAATCAAGTGGAGATGAGCCCGACTTTACATCAAAAAAATC
TGAGGGAATATTGCAAGGCCAATAATATCATGATCACCACACTCAGTTTGGGAGCCGTAGGTGCCGCTGGG
GCACCAATGCAGTTATGCATTCTAAGGTGCTTACCAGATTGCTGTGGCCAGAGGAAAATCTGTTGCCAGGTTA
GTATGAGATGGGTTTACCAGCAAGGCGCAGTCTTGTGGTGAAGTTTCAATGAAGCGAGGATGAAGGAAAACC
TTAGATATTTGATTGGGAACATAACGGCAGAAGACATGGAAAAGATCAGTGAGATTCCACAATCTAGAACAAGCT
CTGCTGCTTTCTTGTATTACCCGACTGGACCTTTCAAACTGAAGAAGAGTTCTGGGATGAGAAGGATTGAAACA
TCAATTATAGATGGTAAGTGAGGACTGTCAAAAAGTAATCAGTTTTTCCCTCCGTTTTG

cor1.2
cds 1-966

Fig 11

ATGGAGAGTAATGGTGTACCTATGATCACTCTCAGTTCCGGCATTCCGGATGCCTGCTTTAGGTATGGGAACAGTT
GAAACAATGGAAAAGGGAACAGAAAGAGAGAAATTGGCGTTTTTGAATGCGATAGAGGTCGGTTACAGACACTTC
GATACAGCTGCTGCATACCAAAGTGAAGAGTGTCTTGGTGAAGCTATAGCTGAAGCACTTCAACTTGGTTAATA
AAATCTCGAGATGAACCTTTCATCACTTCCAAGCTCTGGTGGCTGATGCTCAGCTGATCTTGTCTCTCCCTGCT
CTTCAGAATTCTCTGAGGAATCTCAAATTGGAGTACCTTGATCTATATTTGATACACCATCCGGTAAGCTTGAAG
CCAGGGAAGCTTGTAAACGAAATACCAAAGGATCATATCTTCCAATGGACTACAAATCTGTATGGGCAGCCATG
GAAGAGTGTGAGACCCTTGGCTTCACTAGGGCAATCGGTGTGAGTAATTTCTCATGCAAAAAGCTTCAAGAGTTG
ATGGCAACAGCCAAGATCCCTCCAGTTGTGAATCAAGTGGAGATGAGCCCGACTTTACATCAAAAAAATCTGAGG
GAATATTGCAAGGCCAATAATATCATGATCACTGCACACTCGGTTTTGGGAGCCATAGGTGCTCCATGGGGCAGC
AACGCAGTTATGGATTCTAAGGTGCTTACCAGATTGCTGTGGCAAGAGGAAAATCTGTTGCCAGGTTAGTATG
AGATGGGTTTACCAGCAAGGCGCAGTCTTGTGGTGAAGTTTCAATGAAGCGAGGATGAAGGAAAACCTTAAG
ATATTTGATTCCGAACTAACGGCAGAAGATATGAAAAGATCAGTGAGATTCCGCAATCTAGAACAAGCTCTGCT
GATTTCTTGTATACCCGACTGGACCTTTCAAACTGAAGAAGAGTTCTGGGATGAGAAGGATTGA

cor1.3
cds1-966

Fig 12

ATGGAGAGTAATGGTGTACCTATGATCACTCTCAGTTCCGGCATTCCGGATGCCTGCTTTAGGTATGGGAACAGCT
GAAACAATGGTAAAAGGAACAGAAAGAGAGAAATTGGCGTTTTTGAAGCGATAGAGGTCGGTTACAGACACTTC
GATACAGCTGCTGCATACCAAAGTGAAGAGTGTCTTGGTGAAGCTATAGCTGAAGCACTTCAACTTGGTTAATA
AAATCTCGAGATGAACCTTTCATCACTTCCAAGCTCTGGTGGCTGATGCTCAGCTGATCTTGTCTCTCCCTGCT
CTTCAGAATTCTCTGAGGAATCTTAAATTGGACTATCTTGATCTATATTTGATACACCATCCGGTAAGCTTGAAG
CCAGGGAAGTTTGTAAACGAAATACCAAAGGATCATATCCTTCCAATGGACTACAAATCTGTATGGGCAGCCATG
GAAGAGTGTGAGACCCTTGGCTTCACTAGGGCAATCGGGGTCTGTAATTTCTCATGCAAAAAGCTTCAAGAGTTG
ATGGCAGCAGCCAAGATCCCTCCAGTTGTGAATCAAGTGGAGATGAGCCCGACTTTACATCAAAAAAATCTGAGG
GAATATTGCAAGGCCAATAATATCATGATCACTGCACACTCGGTTTTGGGAGCCATAGGTGCTCCATGGGGCAGC
AATGCAGTTATGGATTCTAAGGTGCTTACCAGATTGCTGTGGCAAGAGGAAAATCTGTTGCCAGGTTAGTATG
AGATGGGTTTACCAGCAAGGCGCAGTCTAGTGGTGAAGTTTCAATGAAGGGAGGATGAAGGAAAACCTTAAG
ATATTTGATTGGGAACATAACGGCAGAGAATATGAAAAGATCAGTGAGATTCCGCAATCTAGAACAAGCTCTGCT
GATTTCTTGTATACCCGACTGGACCTTTCAAACTGAAGAAGAGTTCTGGGATGAGAAGGATTGA

cor1.4
cds1-966

Fig 13

ATGGAGAGTAATGGTGTACCTATGATCACTCTCAGTTCCGGCATTCCGGATGCCTGCTTTAGGTATGGGAACAGCT
GAAACAATGGTAAAAGGAACAGAAAGAGAGAAATTGGCGTTTTTGAAGCGATAGAGGTCGGTTACAGACACTTC
GATACAGCTGCTGCATACCAAAGTGAAGAGTGTCTTGGTGAAGCTATAGCTGAAGCACTTCAACTTGGTTAATA
AAATCTCGAGATGAACCTTTCATCACTTCCAAGCTCTGGTGGCTGATGCTCAGCTGATCTTGTCTCTCCCTGCT

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CTTCAGAAATCTCTGAGGAATCTCAAATTGGAGTATCTTGATCTATATTTGATACACCATCCGGTAAGCTTGAAG
CCAGGGAAATTTGTTAACGAAATACCAAAGGATCATATTCTTCCAATGGACTACAAATCTGTATGGGCAGCCATG
GAAGAGTGTGAGACCCTTGGCTTCACTAGGGCAATCGGTGTCAGTAATTTCTCATGCAAAAAGCTTCAAGAGTTG
ATGGCAGCAGCCAAGATCCCTCCAGTTGTGAATCAAGTGGAGATGAGCCCTACTTTACATCAAAAAAATCTGAGG
GAATATTGCAAGGCCAATAATATCATGATCACTGCACACTCGGTTTTGGGAGCCATAGGTGCTCCATGGGGCAGC
AATGCAGTTATGGATTCTAAGGTGCTTACCAGATTGCTGTGGCAAGAGGAAAAATCTGTTGCCAGGTTAGTATG
AGATGGGTTTACCAGCAAGGCGCGAGTCTTGTGGTGAAGTTTCAATGAAGGGAGGATGAAGGAAAACCTTAAG
ATATTTGATTGGGAACTAACGGCAGAAGATATGGAAAAGATCAGTGAGATTCCGCAATCTAGAACAAGCTCTGCT
GCTTTCTTGTTATCACCGACTGGACCTTTCAAAACGAAGAAGAGTTCTGGGATGAGAAGGATTGA

cor1.5
partial seq

Fig 14

TGTGGTGAATCAGGTGGAGATGTGGCCGACTTTACATCAAAAAAATCTGAGGGAATATTGCAAGGCCAATAATAT
CATGATCACTGCACACTCGGTTTTGGGAGCCATAGGTGCTCCATGGGGCAGCAATGCAGTTATGGATTCTAAGGT
GCTT

cor1.6
partial seq

Fig 15

CTCTGGTGCGCTGATGCTCACGCTGATCTTGTCTCCCTGCTCTTCAGAAATCTCTGAGGAATCTCAAATTGGAC
TACCTTGATCTATATTTGATACACCATCCGGTAAGCTTGAAGCCAGGGAAGCTTGTTAACGAAATACCAAAGGAT
CATATTCTTCCAATGGACTACAAATCTGTATGGGCAGCCATGGAAGAGTGTGAGACCCTTGGCTTCACTAGGGCA
ATCGGTGTCAGTAATTTCTCATGCAAAAAGCTTCAAGAGTTGATGGCAACAGCCAAGATCCCTCCA